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 AGGATGTCCA CTACATGCTC GCGCGCTGA GAGCTCTGC TCTCTCTGC GAAGCGGACA 300
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10023839.122101

SEQ ID N . 2.

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GGT GTC AAT GGA ATC GGA GCG CTA CCT GGT GGC AAG GTC AAG CTG TGT 527
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ATT CCG TAC GTC GAA ATG ACA TTG AGA TTG ATG GAG CGT TTT GGT GTG 671
 Ile Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val
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10023839.122101

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OCT GAG GTA GTG GAG ATG ATG GGA GCG AAG GTT ACA TGG ACC GAG ACT Ala Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr 290 295 300	911
AGC GTA ACT GTT ACT GGC CCA CCG CCG GAG CCA TTT GGG ACG AAA CAC Ser Val Thr Val Thr Gly Phe Pro Arg Glu Pro Phe Gly Arg Lys His 305 310 315	959
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TAC TGC ATC ATC ACG CCG CCG GAG AAG CTG AAC GTG ACG GCG ATC GAC Tyr Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp 385 390 395	1199
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GCC GAG GTC CCC GTC ACC ATC CCG GAC CCT GCG TCC ACC CCG AAG ACC Ala Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr 415 420 425 430	1295
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TAA	1340

F00222T "688E200T

SEQ ID No. 3.

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 Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
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 Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Glu Leu Phe
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 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
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 Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
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 Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
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 Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
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 Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
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 Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
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 Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
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 Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
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 340 345 350
 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
 355 360 365
 Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
 370 375 380
 Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
 385 390 395 400
 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
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10023839-122101

SEQ ID No. 4.

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CTG	AAC	AGT	GAG	GAT	CTC	CAC	TAC	ATG	CTC	GGG	CCC	TTC	AGG	ACT	CTT	191
Leu	Asn	Ser	Glu	Asp	Val	His	Tyr	Met	Leu	Gly	Ala	Leu	Arg	Thr	Leu	
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Gly	Leu	Ser	Val	Glu	Ala	Asp	Lys	Ala	Ala	Lys	Arg	Ala	Val	Val	Val	
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Lys	Ala	Glu	His	Ser	Asp	Ser	Trp	Asp	Arg	Phe	Tyr	Ile	Lys	Gly	Gly	
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1003339-122101

SEQ ID N . 4 (c ntinuation).

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ACT GTG GAA GGT TGT GGC ACC ACC AGT TTG CAG GGT GAT GTG AAG TTT Thr Val Glu Gly Cys Gly Thr Thr Ser Leu Glu Gly Asp Val Lys Phe 275 280 285	863
OCT GAG GTA GTG GAG ATG ATG GGA GCG AAG GTT ACA TGG ACC GAG ACT Ala Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr 290 295 300	911
AAC GTA ACT GTT ACT GGC CCA CCG CCG GAG CCA TTT GCG AGG AAA CAC Ser Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His 305 310 315	959
CTC AAG GCG ATT GAT GTC AAC ATG AAC AAG ATC OCT GAT GTC GCC ATG Leu Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met 320 325 330	1007
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GAC GTG GCT TCC TGG AGA GTA AAG GAG ACC GAG AGG ATG GTT GCG ATC Asp Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile 355 360 365	1103
CGG ACC GAG CTA ACC AAG CTG GCA CCA TCT GTT GAG GAA GCG CCG GAC Arg Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp 370 375 380	1151
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GCC GAG GTC CCC GTC ACC ATC CCG GAC CCT GCG TGC ACC CCG AAG ACC Ala Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr 415 420 425 430	1295
TTC CCC GAC TAC TTC GAT GTG CTG AGC ACT TTC GTC AAG AAT Phe Pro Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn 435 440	1337
TAA	1340

"100839" 12201

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 Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Glu Leu Phe
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10023839.12210.1

SEQ ID No. 6.

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F0122T "6E8E200T

SEQ ID No. 7.

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10023839.12101

SEQUENCE LISTING

<110> DEROSE, Richard
CHAUBET, Nicole
GIGOT, Claude (deceased)

<120> ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
ELEMENT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE
TRANSFORMATION OF PLANTS

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<140> 09/000,062

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 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
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 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu

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Asn	Ser	Glu	Asp	Val	His	Tyr	Met	Leu	Gly	Ala	Leu	Arg	Thr	Leu	Gly	
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ctc	tct	gtc	gaa	gcg	gac	aaa	gct	gcc	aaa	aga	gct	gta	gtt	gtt	ggc	242
Leu	Ser	Val	Glu	Ala	Asp	Lys	Ala	Ala	Lys	Arg	Ala	Val	Val	Val	Gly	
65					70					75						
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Cys	Gly	Gly	Lys	Phe	Pro	Val	Glu	Asp	Ala	Lys	Glu	Glu	Val	Gln	Leu	
80					85					90					95	
ttc	ttg	ggg	aat	gct	gga	act	gca	atg	cgg	cca	ttg	aca	gca	gct	gtt	338
Phe	Leu	Gly	Asn	Ala	Gly	Thr	Ala	Met	Arg	Pro	Leu	Thr	Ala	Ala	Val	
100					105					110						
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Thr	Ala	Ala	Gly	Gly	Asn	Ala	Thr	Tyr	Val	Leu	Asp	Gly	Val	Pro	Arg	
115					120					125						
atg	agg	gag	aga	ccc	att	ggc	gac	ttg	gtt	gtc	gga	ttg	aag	cag	ctt	434
Met	Arg	Glu	Arg	Pro	Ile	Gly	Asp	Leu	Val	Val	Gly	Leu	Lys	Gln	Leu	
130					135					140						
ggc	gca	gat	gtt	gat	tgt	ttc	ctt	ggc	act	gac	tgc	cca	cct	gtt	cgt	482
Gly	Ala	Asp	Val	Asp	Cys	Phe	Leu	Gly	Thr	Asp	Cys	Pro	Pro	Val	Arg	
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Val	Asn	Gly	Ile	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	
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Ser	Ile	Ser	Ser	Gln	Tyr	Leu	Ser	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	
180					185					190						
gct	ctt	ggg	gat	gtg	gag	att	gaa	atc	att	gat	aaa	tta	atc	tcc	att	626
Ala	Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Ile	Asp	Lys	Leu	Ile	Ser	Ile	
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Pro	Tyr	Val	Glu	Met	Thr	Leu	Arg	Leu	Met	Glu	Arg	Phe	Gly	Val	Lys	
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gca	gag	cat	tct	gat	agc	tgg	gac	aga	ttc	tac	att	aag	gga	ggc	caa	722
Ala	Glu	His	Ser	Asp	Ser	Trp	Asp	Arg	Phe	Tyr	Ile	Lys	Gly	Gly	Gln	
225					230					235						
aaa	tac	aag	tcc	cct	aaa	aat	gcc	tat	gtt	gaa	ggc	gat	gcc	tca	agc	770
Lys	Tyr	Lys	Ser	Pro	Lys	Asn	Ala	Tyr	Val	Glu	Gly	Asp	Ala	Ser	Ser	
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qca	agc	tat	ttc	ttg	gct	ggc	gct	gca	att	act	gga	ggg	act	gtg	act	818

Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr	
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gtg gaa ggt tgt ggc acc acc agt ttg cag ggt gat gtg aag ttt gct	866
Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala	
275 280 285	
gag gta ctg gag atg atg gga gcg aag gtt aca tgg acc gag act agc	914
Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser	
290 295 300	
gta act gtt act ggc cca ccg cgg gag cca ttt ggg agg aaa cac ctc	962
Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu	
305 310 315	
aag gcg att gat gtc aac atg aac aag atg cct gat gtc gcc atg act	1010
Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr	
320 325 330 335	
ctt gct gtg gtt gcc ctc ttt gcc gat ggc ccg aca gcc atc aga gac	1058
Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp	
340 345 350	
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Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg	
355 360 365	
acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg gac tac	1154
Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr	
370 375 380	
tgc atc atc acg ccg ccg gag aag ctg aac gtg acg gcg atc gac acg	1202
Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr	
385 390 395	
tac gac gac cac agg atg gcc atg gcc ttc tcc ctt gcc gcc tgt gcc	1250
Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala	
400 405 410 415	
gag gtc ccc gtc acc atc cgg gac cct ggg tgc acc cgg aag acc ttc	1298
Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe	
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Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu	50	55	60
Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys	65	70	75
Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe	85	90	95
Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr	100	105	110
Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met	115	120	125
Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly	130	135	140
Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val	145	150	155
Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser	165	170	175
Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala	180	185	190
Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro	195	200	205
Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala	210	215	220
Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys	225	230	235
Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala	245	250	255
Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val	260	265	270
Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu	275	280	285
Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val	290	295	300

Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
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Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
355 360 365

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
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Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
20 25 30

cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg 146
Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
35 40 45

aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt 194
Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
50 55 60

ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc 242

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Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly	
65 70 75	
tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc	290
Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu	
80 85 90 95	
ttc ttg ggg aat gct gga atc gca atg cgg tcc ttg aca gca gct gtt	338
Phe Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val	
100 105 110	
act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga	386
Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg	
115 120 125	
atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt	434
Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu	
130 135 140	
ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt	482
Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg	
145 150 155	
gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc	530
Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly	
160 165 170 175	
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Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu	
180 185 190	
gct ctt ggg gat gtg gag att gaa atc att gat aaa tta atc tcc att	626
Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile	
195 200 205	
ccg tac gtc gaa atg aca ttg aga ttg atg gag cgt ttt ggt gtg aaa	674
Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys	
210 215 220	
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Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln	
225 230 235	
aaa tac aag tcc ect aaa aat gcc tat gtt gaa ggt gat gcc tca agc	770
Lys Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser	
240 245 250 255	
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Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr	
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Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala	
275 280 285	

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Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser	
290 295 300	
gta act gtt act ggc cca ccg cgg gag cca ttt ggg agg aaa cac ctc	962
Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu	
305 310 315	
aag gcg att gat gtc aac atg aac aag atg cct gat gtc gcc atg act	1010
Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr	
320 325 330 335	
ctt gct gtg gtt gcc ctc ttt gcc gat ggc ccg aca gcc atc aga gac	1058
Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp	
340 345 350	
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Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg	
355 360 365	
acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg gac tac	1154
Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr	
370 375 380	
tgc atc atc acg ccg ccg gag aag ctg aac gtg acg gcg atc gac acg	1202
Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr	
385 390 395	
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Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala	
400 405 410 415	
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Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe	
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 35 40 45

Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
 50 55 60
 Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
 65 70 75 80
 Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
 85 90 95
 Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val Thr
 100 105 110
 Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
 115 120 125
 Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
 130 135 140
 Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
 145 150 155 160
 Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
 165 170 175
 Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala
 180 185 190
 Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
 195 200 205
 Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
 210 215 220
 Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
 225 230 235 240
 Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
 245 250 255
 Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
 260 265 270
 Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
 275 280 285
 Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
 290 295 300
 Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
 305 310 315 320
 Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
 325 330 335
 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val

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Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr		
355	360	365
Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys		
370	375	380
Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr		
385	390	395 400
Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu		
405	410	415
Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro		
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Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn		
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 ccattatctt gtttcttcgc cgaatgatct tccgtataaa gatttttaggt tagagatgaa 180
 tcgtatagct agatttcac accagatagt ttctttgtct agaatctctg aaattctcga 240
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 tttcttgatt atgcgattgc aattagggat tttctttggg tttgtgttga tcttacgata 360
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 cgggttttgg cccattccag tttgaaaata aacgtccgtc ttttaagttt gctggatcga 180
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37

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<400> 14
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25

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33

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33

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34

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<210> 19

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18

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<210> 22
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20

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